



Application No.: 09/555,093 *Applicant*

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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SEQUENCE LISTING

<110> Napier, Johnathan A.

<120> Desaturase Genes and their Use

<130> 000487.00001

<140> US 09/555,093

<141> 2000-08-22

<150> UK 9724783.7

<151> 1997-11-24

<150> PCT/GB98/03507

<151> 1998-11-24

<160> 8

<170> FastSEQ for Windows Version 4.0

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<211> 1462

<212> DNA

<213> C. elegans

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Val Asp Gly Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His 25
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cca gga gga gct gtt att gaa caa tat aga aat tcg gat gct act cat 145
Pro Gly Gly Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His 45
30 35 40

att ttc cac gct ttc cac gaa gga tct tct cag gct tat aag caa ctt 193
Ile Phe His Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu 60
50 55

gac ctt ctg aaa aag cac gga gag cac gat gaa ttc ctt gag aaa caa 241
Asp Leu Leu Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln 75
65 70

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Leu Glu Lys Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp

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Arg Gln Lys Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr			
110	115	120	
ttc ctg ttt aaa gcg att tca aca ctt tca att atg gca ttt gca ttt			433
Phe Leu Phe Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe			
130	135	140	
tat ctt cag tat ctt gga tgg tat att act tct gca tgt tta tta gca			481
Tyr Leu Gln Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala			
145	150	155	
ctt gca tgg caa caa ttc gga tgg tta aca cat gag ttc tgc cat caa			529
Leu Ala Trp Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln			
160	165	170	
cag cca aca aag aac aga cct ttg aat gat act att tct ttg ttc ttt			577
Gln Pro Thr Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe			
175	180	185	
ggt aat ttc tta caa gga ttt tca aga gat tgg tgg aag gac aag cat			625
Gly Asn Phe Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His			
190	195	200	
aac act cat cac gct gcc aca aat gta att gat cat gac ggt gat atc			673
Asn Thr His His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile			
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gac ttg gca cca ctt ttc gca ttt att cca gga gat ttg tgc aag tat			721
Asp Leu Ala Pro Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr			
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Leu Tyr Phe Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly			
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cag tca gtt caa tgg gta ttc aaa gag aat caa atg gag tac aag gtc			865
Gln Ser Val Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val			
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tat caa aga aat gca ttc tgg gag caa gca aca att gtt gga cat tgg			913
Tyr Gln Arg Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp			
290	295	300	
gct tgg gta ttc tat caa ttg ttc tta tta cca aca tgg cca ctt cgg			961

Ala Trp Val Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg
305 310 315

gtt gct tat ttc att att tca caa atg gga gga ggc ctt ttg att gct 1009
Val Ala Tyr Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala
320 325 330

cac gta gtc act ttc aac cat aac tct gtt gat aag tat cca gcc aat 1057
His Val Val Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn
335 340 345

tct cga att tta aac aac ttc gcc gct ctt caa att ttg acc aca cgc 1105
Ser Arg Ile Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg
350 355 360 365

aac atg act cca tct cca ttc att gat tgg ctt tgg ggt gga ctc aat 1153
Asn Met Thr Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn
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tat cag atc gag cac cac ttg ttc cca aca atg cca cgt tgc aat ctg 1201
Tyr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu
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aat gct tgc gtg aaa tat gtg aaa gaa tgg tgc aaa gag aat aat ctt 1249
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400 405 410

cct tac ctc gtc gat gac tac ttt gac gga tat gca atg aat ttg caa 1297
Pro Tyr Leu Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln
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caa ttg aaa aat atg gct gag cac att caa gct aaa gct gcc t 1340
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430 435 440

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<213> C. elegans

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35 40 45
Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu
50 55 60
Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys
65 70 75 80

Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val
 85 90 95
 Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys
 100 105 110
 Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe
 115 120 125
 Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln
 130 135 140
 Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp
 145 150 155 160
 Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr
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 Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe
 180 185 190
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 His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala
 210 215 220
 Pro Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser
 225 230 235 240
 Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe
 245 250 255
 Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val
 260 265 270
 Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg
 275 280 285
 Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val
 290 295 300
 Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr
 305 310 315 320
 Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala His Val Val
 325 330 335
 Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile
 340 345 350
 Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr
 355 360 365
 Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile
 370 375 380
 Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys
 385 390 395 400
 Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu
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<213> Artificial Sequence

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<212> PRT

<213> C. elegans

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35 40 45
Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu
50 55 60
Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys
65 70 75 80
Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val
85 90 95
Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys
100 105 110
Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe
115 120 125
Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln
130 135 140
Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp
145 150 155 160
Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr
165 170 175
Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe
180 185 190
Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His
195 200 205
His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala
210 215 220
Phe Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser
225 230 235 240
Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe
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Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val
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Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg
275 280 285
Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val
290 295 300
Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr

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 Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile 335
 Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr 350
 Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile 365
 Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys 380
 Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu 395
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 Arg Gly Ile Ile Thr Thr Arg Gly Ser Ser Asn Ala Leu Asp Ile Leu 60
 Tyr Phe Tyr Arg Asn Ser Asp Ala Thr His Ile Phe His Ala Phe His 80
 Glu Gly Ser Ser Gln Ala Tyr Lys Lys Gln Leu Asp Leu Leu Lys Lys His 95
 Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys Arg Leu Asp 110
 Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val Gln Glu Lys 125
 Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys Leu His Asp Asp 140
 Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe Lys Ala Ile Ser 160
 Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln Tyr Leu Gly Trp 175
 Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp Gln Gln Phe Gly 190
 Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr Lys Asn Arg Pro 205
 Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe Leu Gln Gly Phe 220
 Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His His Ala Ala Thr 240
 Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala Phe Leu Phe Ala

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 Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val Gln Trp Val Phe
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 Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg Asn Ala Phe Trp
 305 310 315 320
 Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val Phe Tyr Gln Leu
 325 330 335
 Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr Phe Ile Ile Ser
 340 345 350
 Gln Met Gly Gly Gly Leu Leu Ile Ala His Val Val Thr Phe Asn His
 355 360 365
 Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile Leu Asn Asn Phe
 370 375 380
 Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr Pro Ser Pro Phe
 385 390 395 400
 Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
 405 410 415
 Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys Met Lys Tyr Val
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 Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu Val Asp Asp Tyr
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 35 40 45
 Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu
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 Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys
 65 70 75 80
 Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val
 85 90 95
 Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys
 100 105 110
 Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe
 115 120 125
 Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln
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 Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp

145 150 155 160
 Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr
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 Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe
 180 185 190
 Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His
 195 200 205
 His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala
 210 215 220
 Pro Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser
 225 230 235 240
 Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe
 245 250 255
 Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val
 260 265 270
 Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg
 275 280 285
 Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val
 290 295 300
 Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr
 305 310 315 320
 Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala His Val Val
 325 330 335
 Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile
 340 345 350
 Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr
 355 360 365
 Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile
 370 375 380
 Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys
 385 390 395 400
 Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu
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 <213> C. elegans

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 35 40 45
 Ser Leu Ala Gly Gln Glu Val Thr Asp Ala Phe Val Ala Phe His Pro
 50 55 60
 Ala Ser Thr Trp Lys Asn Leu Asp Lys Phe Phe Thr Gly Tyr Tyr Leu
 65 70 75 80
 Lys Asp Tyr Ser Val Ser Glu Val Ser Lys Asp Tyr Arg Lys Leu Val

His Pro Gly Gly

1